



1/47

1 GTCTTCCACCATCGCTGGGCTTCTTCTGTGGCGTGTCTCTGTCTCGTCCGCGCTG 60
-----+-----+-----+-----+-----+
CAGGAAGGTGGTACGTGAGCGACCCGAAGAAGAGACACCGCACAAAGAGACGAGCGCGGAC
M H S L G F F S V A C S L L A A A -
CGCTGCTCCCGGCTCTCGGAGGCGCGCGCGCGCGCGCGCTTCGAGTCCGGACTCG 120
-----+-----+-----+-----+-----+
GCGACGAGGCGCCAGGAGCGCTCCGCGGCGCGCGCGCGCGGAGCTCAGGCCCTGAGC
L L P G P R E A P A A A A A F E S G L D -
ACCTCTCGGACGCGGAGCCCGACGCGGCGGAGGCCACGGCTTATGCAAGCAAAGATCTGG 180
-----+-----+-----+-----+-----+
TGGAGAGCCTGCGCCTCGGCTGCGCGCGCTCCGGTGCGCGAATACGTTCTGTAGACC
L S D A E P D A G E A T A Y A S K D L E -
AGGAGCAGTTACGGTCTGTGTCAGTGATGAAGTCACTGACTGTACTCTACCCAGAAT 240
-----+-----+-----+-----+-----+
TCCTCGTCAATGCCAGACACAGGTCACATCTACTTGAGTACTGACATGAGATGGGTCTTA
E Q L R S V S S V D E L M T V L Y P E Y -
ATTGGAAAATGTACAAGTGTGCTAGCTAAGGAAGGAGGCTGGCAACATAACAGAGAACAGG 300
-----+-----+-----+-----+-----+
TAACCTTTTACATGTTACACAGTCGATTCTCTTCCCTCCGACCGTTGTATGTCTCTGTCC
W K M Y K C Q L R K G G W Q H N R E Q A -
CCAACTCAACTCAAGGACAGAGAGACTATAAAATTTGCTGCAGCACATTATAATACAG

FIG. 1A

FIG. 1B

3/47

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661  TTTACAGACAAGTTCATTTCCATTATTAGACGTTCCCTGCCAGCAACACTACCACAGTGTC
720  AAATGCTCTGTTCAAGTAAGGTAATAATCTGCAAGGGACGGTCGTTGTGATGGTGTACACAG
    Y R Q V H S I I R R S L P A T L P Q C Q -
721  AGGCAGCGAACAAGACCTGCCCCACCAATTACATGTGGAATAATCACATCTGCAGATGCC
780  TCCGTCGCTTGTCTGGACGGGGTGGTTAATGTACACCTTATTAGTGTAGACGTCCTACGG
    A A N K T C P T N Y M W N N H I C R C L -
781  TGGCTCAGGAAGATTTTATGTTTTCCTCGGATGCTGGAGATGACTCAACAGATGGATTCC
840  ACCGAGTCCTTCTAATAAATACAAAAGGAGCCTACGACCTCTACTGAGTTGTCTACCTAAGG
    A Q E D F M F S S D A G D S T D G F H -
841  ATGACATCTGTGGACCAACAAGAGCTGGATGAAGAGACCTGTCTGAGTGTCTGCAGAG
900  TACTGTAGACACCTGGTTTGTTCCTCGACCTACTTCTCTGGACAGTCAACACAGACGCTC
    D I C G P N K E L D E E T C Q C V C R A -
901  CGGGGCTTCGGCCCTGCCAGCTGTGGACCCCAAGAACTAGACAGAACTCATGCCAGT
960  GCCCCGAAGCCGGGTCGACACCTGGGGTGTCTTCTTGATCTGTCTTTGAGTACGGTCA
    G L R P A S C G P H K E L D R N S C Q C -
961  GTGTCTGTAAAAACAACCTCTTCCCCAGCCAATGTGGGGCCAACCGAGAATTGTGATGAAA
1020  CACAGACATTTTGTGAGAAAGGGTCGGTTACACCCCGGTTGGCTCTTAAACTACTTT
```

FIG. 1C

4/47

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V C K N K L F P S Q C G A N R E F D E N -
1021 ACATGCCAGTGTATGTAAGAACCTGCCCCAGAAATCAACCCCTAAATCCTGGAA
-----+-----+-----+-----+-----+
TGTTACGGTCACACATACATTTCTTGGACGGGTCTTTAGTTGGGGATTTAGGACCTT
T C Q C V C K R T C P R N Q P L N P G K -
1081 AATGTGCTGTGAATGTACAGAAAGTCCACAGAAATGCTTGTAAAGGAAGAGTTCC
-----+-----+-----+-----+-----+
TTACACGGACACTTACATGTCTTTACAGGTGTCTTTACGAACAATTTCCCTTCTCAAGG
C A C E C T E S P Q K C L L K G K K F H -
1141 ACCACCAACATGCAGCTGTTACAGACGGCCCATGTACGAACCCGAGAGGCTGTGAGC
-----+-----+-----+-----+-----+
TGGTGGTTTGACGTCGACAAATGTCTGCCGGTACATGCTTGGCGGTCTTCCGAACACTCG
H Q T C S C Y R R P C T N R Q K A C E P -
1201 CAGGATTTTCATATAGTGAAGAAGTGTGTCGTTGTGTCCTTCATATTTGGCAAAGACCAC
-----+-----+-----+-----+-----+
GTCCTAAAAGTATATCACTTCTTCACACAGCAACACAGGGAAGTATAACCGTTTCTGTG
G F S Y S E E V C R C V P S Y W Q R P Q -
AAATGAGCTAAGATTGTACTGTTTCCAGTTCATCGATTTTCTATTATGGAAAACGTGTG
```

FIG. 1D

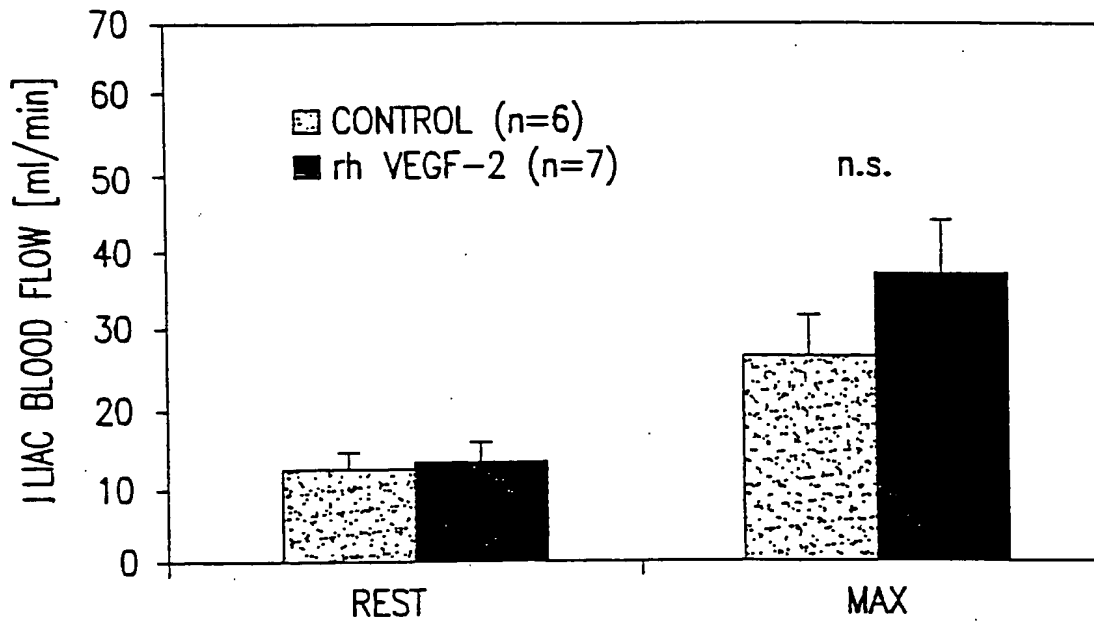
[illegible]

FIG. 1E

33/47

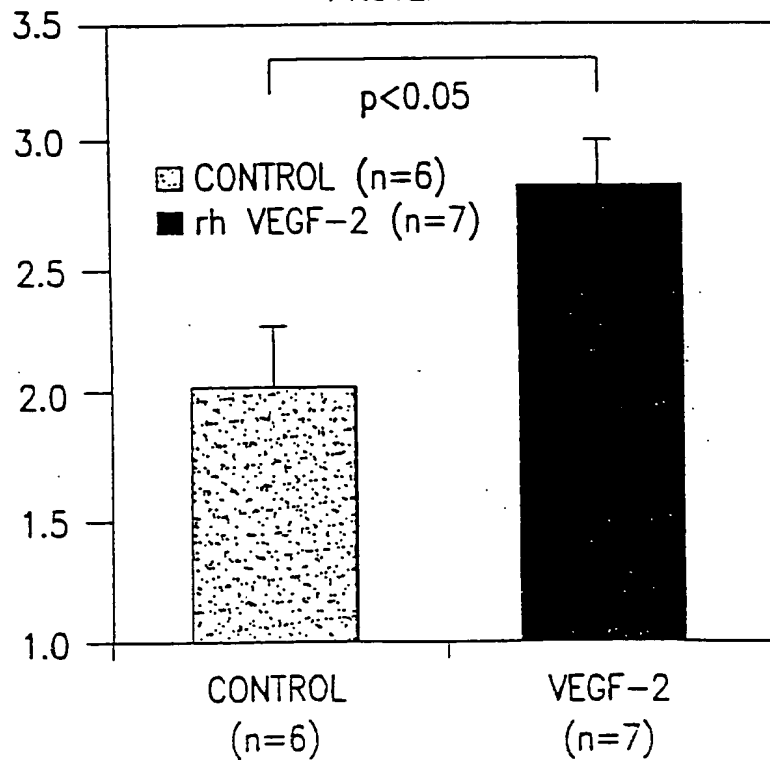
ILIAC BLOOD FLOW
-PROTEIN I.A.-

FIG.25D

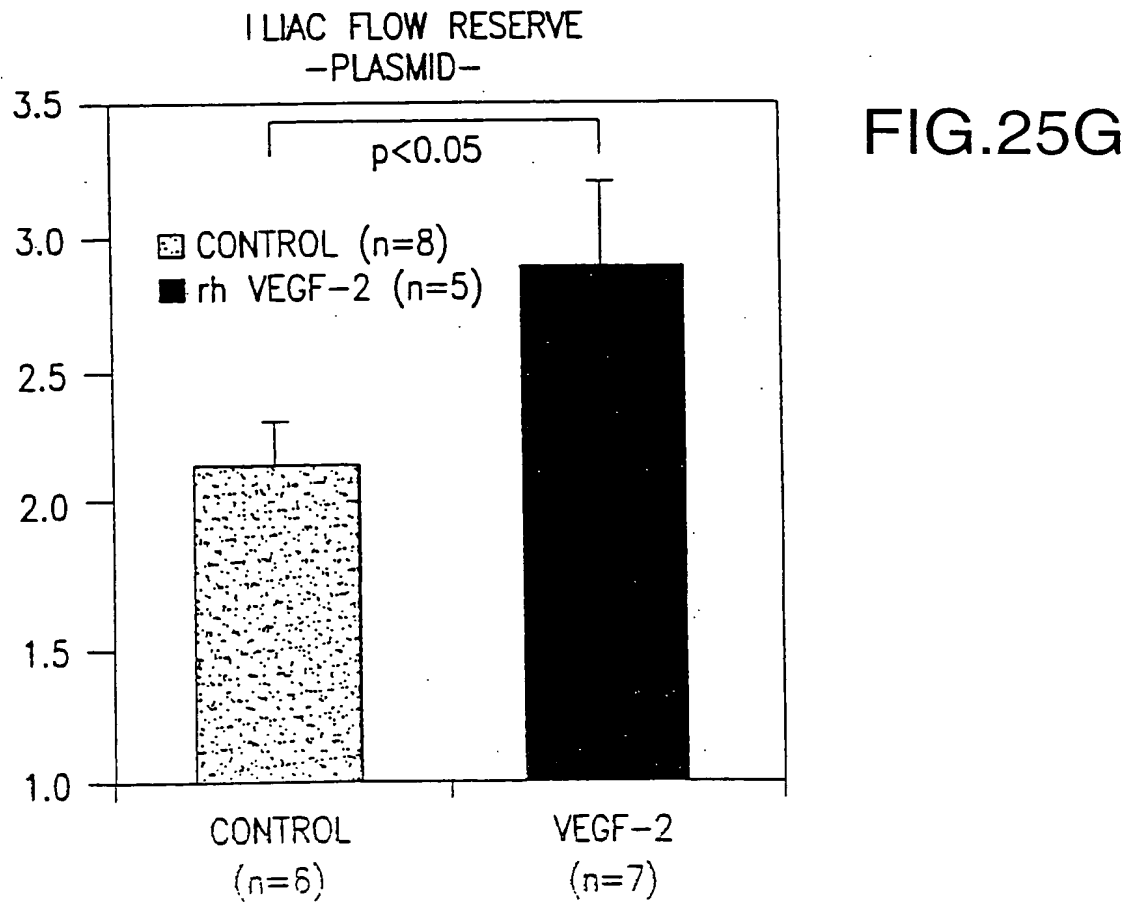
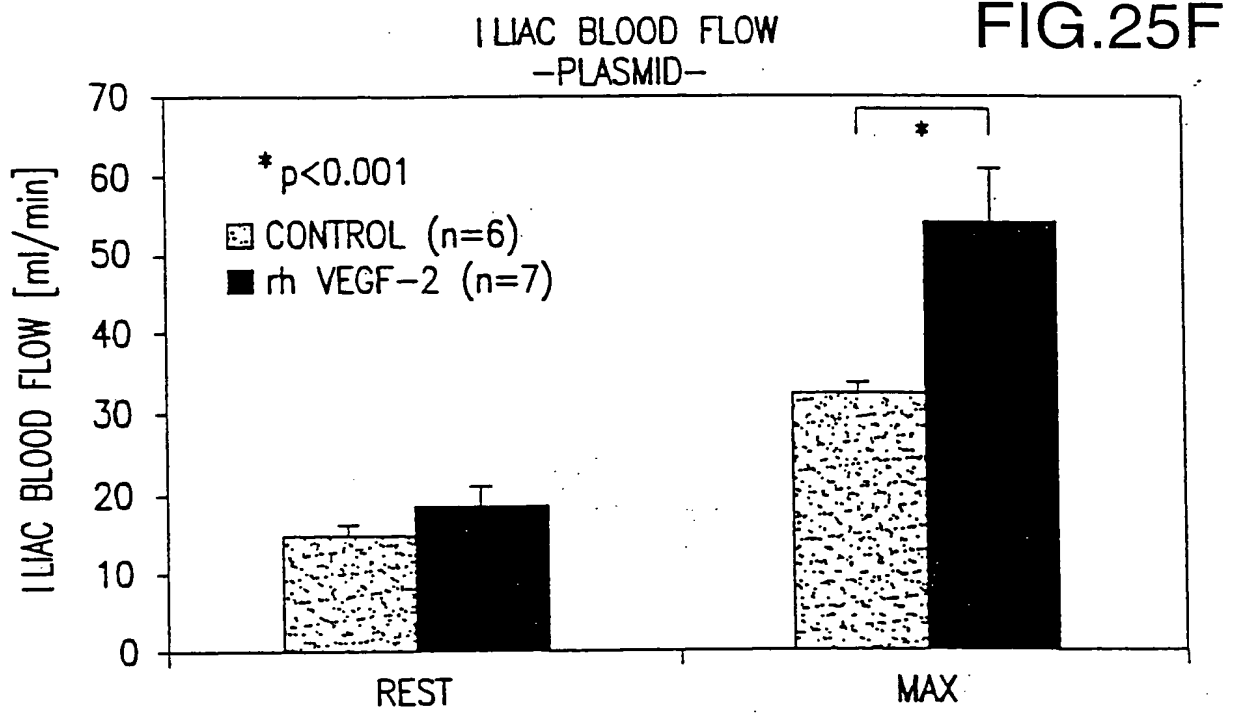


ILIAC FLOW RESERVE
-PROTEIN I.A.-

FIG.25E



34/47



35/47

FIG.25H

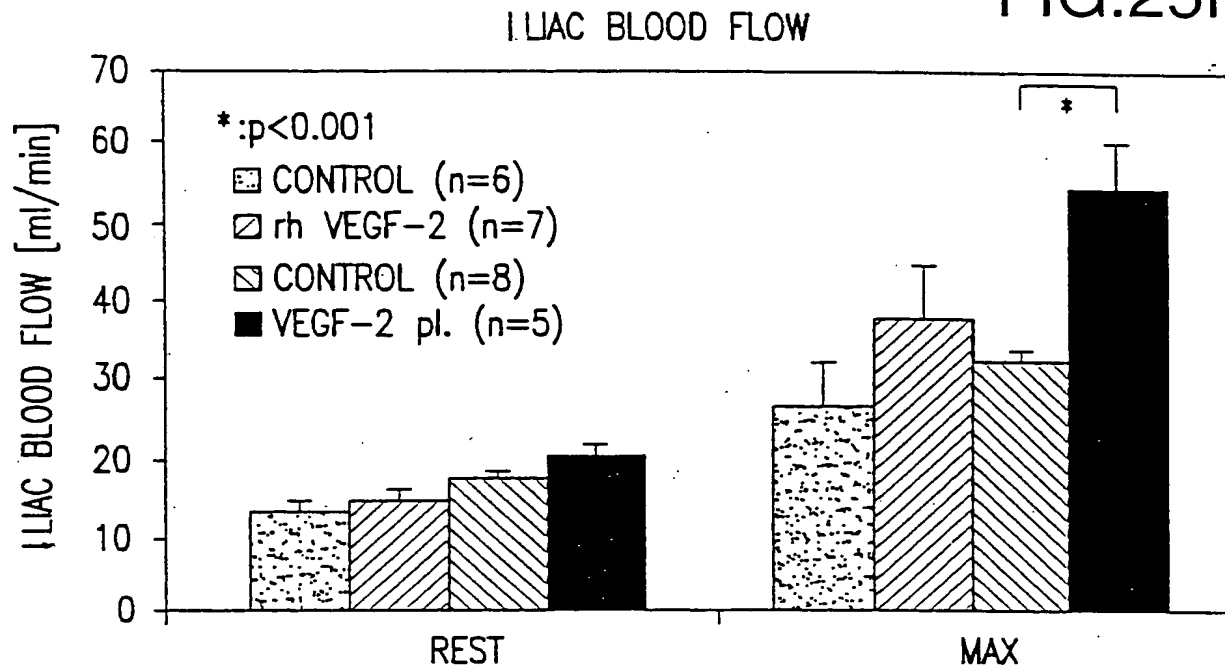


FIG.25I

